



ALLE0004-100sequencelisting.txt
SEQUENCE LISTING

<110> Li, Shengwen
Kei, Aoki R.
Steward, Lance E.
France, Joe

<120> Rescue Agents for Treating a Botulinum Toxin Intoxication

<130> ALLE0004-100

<140> 10/715,810
<141> 2003-11-17

<160> 121

<170> PatentIn version 3.2

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<223> chemically synthesized peptide

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<400> 1
Glu Xaa Xaa His
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<223> Xaa is any amino acid.

<400> 2
Gly Thr Xaa Xaa Asn
1 5

<210> 3
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<220>

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<400> 3

Arg Gly Ser His His His His His His Gly Ser Gly Thr
1 5 10

<210> 4

<211> 1302

<212> PRT

<213> Clostridium botulinum

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Met Pro Phe Val Asn Lys Gln Phe Asn Tyr Lys Asp Pro Val Asn Gly
1 5 10 15

Val Asp Ile Ala Tyr Ile Lys Ile Pro Asn Ala Gly Gln Met Gln Pro
20 25 30

Val Lys Ala Phe Lys Ile His Asn Lys Ile Trp Val Ile Pro Glu Arg
35 40 45

Asp Thr Phe Thr Asn Pro Glu Glu Gly Asp Leu Asn Pro Pro Pro Glu
50 55 60

Ala Lys Gln Val Pro Val Ser Tyr Tyr Asp Ser Thr Tyr Leu Ser Thr
65 70 75 80

Asp Asn Glu Lys Asp Asn Tyr Leu Lys Gly Val Thr Lys Leu Phe Glu
85 90 95

Arg Ile Tyr Ser Thr Asp Leu Gly Arg Met Leu Leu Thr Ser Ile Val
100 105 110

Arg Gly Ile Pro Phe Trp Gly Gly Ser Thr Ile Asp Thr Glu Leu Lys
115 120 125

Val Ile Asp Thr Asn Cys Ile Asn Val Ile Gln Pro Asp Gly Ser Tyr
130 135 140

Arg Ser Glu Glu Leu Asn Leu Val Ile Ile Gly Pro Ser Ala Asp Ile
145 150 155 160

Ile Gln Phe Glu Cys Lys Ser Phe Gly His Glu Val Leu Asn Leu Thr
165 170 175

Arg Asn Gly Tyr Gly Ser Thr Gln Tyr Ile Arg Phe Ser Pro Asp Phe
180 185 190

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Thr Phe Gly Phe Glu Glu Ser Leu Glu Val Asp Thr Asn Pro Leu Leu
195 200 205

Gly Ala Gly Lys Phe Ala Thr Asp Pro Ala Val Thr Leu Ala His Glu
210 215 220

Leu Ile Tyr Ala Gly His Arg Leu Tyr Gly Ile Ala Ile Asn Pro Asn
225 230 235 240

Arg Val Phe Lys Val Asn Thr Asn Ala Tyr Tyr Glu Met Ser Gly Leu
245 250 255

Glu Val Ser Phe Glu Glu Leu Arg Thr Phe Gly Gly His Asp Ala Lys
260 265 270

Phe Ile Asp Ser Leu Gln Glu Asn Glu Phe Arg Leu Tyr Tyr Tyr Asn
275 280 285

Lys Phe Lys Asp Ile Ala Ser Thr Leu Asn Lys Ala Lys Ser Ile Val
290 295 300

Gly Thr Thr Ala Ser Leu Gln Tyr Met Lys Asn Val Phe Lys Glu Lys
305 310 315 320

Tyr Leu Leu Ser Glu Asp Thr Ser Gly Lys Phe Ser Val Asp Lys Leu
325 330 335

Lys Phe Asp Lys Leu Tyr Lys Met Leu Thr Glu Ile Tyr Thr Glu Asp
340 345 350

Asn Phe Val Lys Phe Phe Lys Val Leu Asn Arg Lys Thr Tyr Leu Asn
355 360 365

Phe Asp Lys Ala Val Phe Lys Ile Asn Ile Val Pro Lys Val Asn Tyr
370 375 380

Thr Ile Tyr Asp Gly Phe Asn Leu Arg Asn Thr Asn Leu Ala Ala Asn
385 390 395 400

Phe Asn Gly Gln Asn Thr Glu Ile Asn Asn Met Asn Phe Thr Lys Leu
405 410 415

Lys Asn Phe Thr Gly Leu Phe Glu Phe Tyr Lys Leu Leu Cys Val Arg
420 425 430

Gly Ile Ile Thr Ser Lys Thr Lys Ser Leu Asp Lys Gly Tyr Asn Lys
435 440 445

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Ala Leu Asn Asp Leu Cys Ile Lys Val Asn Asn Trp Asp Leu Phe Phe
450 455 460

Ser Pro Ser Glu Asp Asn Phe Thr Asn Asp Leu Asn Lys Gly Glu Glu
465 470 475 480

Ile Thr Ser Asp Thr Asn Ile Glu Ala Ala Glu Glu Asn Ile Ser Leu
485 490 495

Asp Leu Ile Gln Gln Tyr Tyr Leu Thr Phe Asn Phe Asp Asn Glu Pro
500 505 510

Glu Asn Ile Ser Ile Glu Asn Leu Ser Ser Asp Ile Ile Gly Gln Leu
515 520 525

Glu Leu Met Pro Asn Ile Glu Arg Phe Pro Asn Gly Lys Lys Tyr Glu
530 535 540

Leu Asp Lys Tyr Thr Met Phe His Tyr Leu Arg Ala Gln Glu Phe Glu
545 550 555 560

His Gly Lys Ser Arg Ile Ala Leu Thr Asn Ser Val Asn Glu Ala Leu
565 570 575

Leu Asn Pro Ser Arg Val Tyr Thr Phe Phe Ser Ser Asp Tyr Val Lys
580 585 590

Lys Val Asn Lys Ala Thr Glu Ala Ala Met Phe Leu Gly Trp Val Glu
595 600 605

Gln Leu Val Tyr Asp Phe Thr Asp Glu Thr Ser Glu Val Ser Thr Thr
610 615 620

Asp Lys Ile Ala Asp Ile Thr Ile Ile Ile Pro Tyr Ile Gly Pro Ala
625 630 635 640

Leu Asn Ile Gly Asn Met Leu Tyr Lys Asp Asp Phe Val Gly Ala Leu
645 650 655

Ile Phe Ser Gly Ala Val Ile Leu Leu Glu Phe Ile Pro Glu Ile Ala
660 665 670

Ile Pro Val Leu Gly Thr Phe Ala Leu Val Ser Tyr Ile Ala Asn Lys
675 680 685

Val Leu Thr Val Gln Thr Ile Asp Asn Ala Leu Ser Lys Arg Asn Glu

690

695

700

Lys Trp Asp Glu Val Tyr Lys Tyr Ile Val Thr Asn Trp Leu Ala Lys
705 710 715 720

Val Asn Thr Gln Ile Asp Leu Ile Arg Lys Lys Met Lys Glu Ala Leu
725 730 735

Glu Asn Gln Ala Glu Ala Thr Lys Ala Ile Ile Asn Tyr Gln Tyr Asn
740 745 750

Gln Tyr Thr Glu Glu Glu Lys Asn Asn Ile Asn Phe Asn Ile Asp Asp
755 760 765

Leu Ser Ser Lys Leu Asn Glu Ser Ile Asn Lys Ala Met Ile Asn Ile
770 775 780

Asn Lys Phe Leu Asn Gln Cys Ser Val Ser Tyr Leu Met Asn Ser Met
785 790 795 800

Ile Pro Tyr Gly Val Lys Arg Leu Glu Asp Phe Asp Ala Ser Leu Lys
805 810 815

Asp Ala Leu Leu Lys Tyr Ile Tyr Asp Asn Arg Gly Thr Leu Ile Gly
820 825 830

Gln Val Asp Arg Leu Lys Asp Lys Val Asn Asn Thr Leu Ser Thr Asp
835 840 845

Ile Pro Phe Gln Leu Ser Lys Tyr Val Asp Asn Gln Arg Leu Leu Ser
850 855 860

Thr Phe Thr Glu Tyr Ile Lys Asn Ile Ile Asn Thr Ser Ile Leu Asn
865 870 875 880

Leu Arg Tyr Glu Ser Asn His Leu Ile Asp Leu Ser Arg Tyr Ala Ser
885 890 895

Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp Pro Ile Asp Lys Asn
900 905 910

Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys Ile Glu Val Ile Leu
915 920 925

Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe Ser Thr Ser
930 935 940

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Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser Ile Ser Leu Asn Asn
 945 950 955 960
 Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn Ser Gly Trp Lys Val
 965 970 975
 Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu Gln Asp Thr Gln Glu
 980 985 990
 Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln Met Ile Asn Ile Ser
 995 1000 1005
 Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile Thr Asn Asn Arg
 1010 1015 1020
 Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu Ile Asp Gln
 1025 1030 1035
 Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn Asn Ile
 1040 1045 1050
 Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile Trp
 1055 1060 1065
 Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu
 1070 1075 1080
 Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys
 1085 1090 1095
 Asp Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met
 1100 1105 1110
 Leu Asn Leu Tyr Asp Pro Asn Lys Tyr Val Asp Val Asn Asn Val
 1115 1120 1125
 Gly Ile Arg Gly Tyr Met Tyr Leu Lys Gly Pro Arg Gly Ser Val
 1130 1135 1140
 Met Thr Thr Asn Ile Tyr Leu Asn Ser Ser Leu Tyr Arg Gly Thr
 1145 1150 1155
 Lys Phe Ile Ile Lys Lys Tyr Ala Ser Gly Asn Lys Asp Asn Ile
 1160 1165 1170
 Val Arg Asn Asn Asp Arg Val Tyr Ile Asn Val Val Val Lys Asn
 1175 1180 1185

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Lys Glu Tyr Arg Leu Ala Thr Asn Ala Ser Gln Ala Gly Val Glu
1190 1195 1200

Lys Ile Leu Ser Ala Leu Glu Ile Pro Asp Val Gly Asn Leu Ser
1205 1210 1215

Gln Val Val Val Met Lys Ser Lys Asn Asp Gln Gly Ile Thr Asn
1220 1225 1230

Lys Cys Lys Met Asn Leu Gln Asp Asn Asn Gly Asn Asp Ile Gly
1235 1240 1245

Phe Ile Gly Phe His Gln Phe Asn Asn Ile Ala Lys Leu Val Ala
1250 1255 1260

Ser Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser Arg Thr Leu
1265 1270 1275

Gly Cys Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp Gly Glu
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Arg Pro Leu His His His His His His
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<210> 5
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<213> Clostridium botulinum

<400> 5

Met Pro Phe Val Asn Lys Gln Phe Asn Tyr Lys Asp Pro Val Asn Gly
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Val Asp Ile Ala Tyr Ile Lys Ile Pro Asn Ala Gly Gln Met Gln Pro
20 25 30

Val Lys Ala Phe Lys Ile His Asn Lys Ile Trp Val Ile Pro Glu Arg
35 40 45

Asp Thr Phe Thr Asn Pro Glu Glu Gly Asp Leu Asn Pro Pro Pro Glu
50 55 60

Ala Lys Gln Val Pro Val Ser Tyr Tyr Asp Ser Thr Tyr Leu Ser Thr
65 70 75 80

Asp Asn Glu Lys Asp Asn Tyr Leu Lys Gly Val Thr Lys Leu Phe Glu
85 90 95

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Arg Ile Tyr Ser Thr Asp Leu Gly Arg Met Leu Leu Thr Ser Ile Val
100 105 110

Arg Gly Ile Pro Phe Trp Gly Gly Ser Thr Ile Asp Thr Glu Leu Lys
115 120 125

Val Ile Asp Thr Asn Cys Ile Asn Val Ile Gln Pro Asp Gly Ser Tyr
130 135 140

Arg Ser Glu Glu Leu Asn Leu Val Ile Ile Gly Pro Ser Ala Asp Ile
145 150 155 160

Ile Gln Phe Glu Cys Lys Ser Phe Gly His Glu Val Leu Asn Leu Thr
165 170 175

Arg Asn Gly Tyr Gly Ser Thr Gln Tyr Ile Arg Phe Ser Pro Asp Phe
180 185 190

Thr Phe Gly Phe Glu Glu Ser Leu Glu Val Asp Thr Asn Pro Leu Leu
195 200 205

Gly Ala Gly Lys Phe Ala Thr Asp Pro Ala Val Thr Leu Ala His Glu
210 215 220

Leu Ile His Ala Gly His Arg Leu Tyr Gly Ile Ala Ile Asn Pro Asn
225 230 235 240

Arg Val Phe Lys Val Asn Thr Asn Ala Tyr Tyr Glu Met Ser Gly Leu
245 250 255

Glu Val Ser Phe Glu Glu Leu Arg Thr Phe Gly Gly His Asp Ala Lys
260 265 270

Phe Ile Asp Ser Leu Gln Glu Asn Glu Phe Arg Leu Tyr Tyr Tyr Asn
275 280 285

Lys Phe Lys Asp Ile Ala Ser Thr Leu Asn Lys Ala Lys Ser Ile Val
290 295 300

Gly Thr Thr Ala Ser Leu Gln Tyr Met Lys Asn Val Phe Lys Glu Lys
305 310 315 320

Tyr Leu Leu Ser Glu Asp Thr Ser Gly Lys Phe Ser Val Asp Lys Leu
325 330 335

Lys Phe Asp Lys Leu Tyr Lys Met Leu Thr Glu Ile Tyr Thr Glu Asp
340 345 350

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Asn Phe Val Lys Phe Phe Lys Val Leu Asn Arg Lys Thr Tyr Leu Asn
355 360 365

Phe Asp Lys Ala Val Phe Lys Ile Asn Ile Val Pro Lys Val Asn Tyr
370 375 380

Thr Ile Tyr Asp Gly Phe Asn Leu Arg Asn Thr Asn Leu Ala Ala Asn
385 390 395 400

Phe Asn Gly Gln Asn Thr Glu Ile Asn Asn Met Asn Phe Thr Lys Leu
405 410 415

Lys Asn Phe Thr Gly Leu Phe Glu Phe Tyr Lys Leu Leu Cys Val Arg
420 425 430

Gly Ile Ile Thr Ser Lys Thr Lys Ser Leu Asp Lys Gly Tyr Asn Lys
435 440 445

Ala Leu Asn Asp Leu Cys Ile Lys Val Asn Asn Trp Asp Leu Phe Phe
450 455 460

Ser Pro Ser Glu Asp Asn Phe Thr Asn Asp Leu Asn Lys Gly Glu Glu
465 470 475 480

Ile Thr Ser Asp Thr Asn Ile Glu Ala Ala Glu Glu Asn Ile Ser Leu
485 490 495

Asp Leu Ile Gln Gln Tyr Tyr Leu Thr Phe Asn Phe Asp Asn Glu Pro
500 505 510

Glu Asn Ile Ser Ile Glu Asn Leu Ser Ser Asp Ile Ile Gly Gln Leu
515 520 525

Glu Leu Met Pro Asn Ile Glu Arg Phe Pro Asn Gly Lys Lys Tyr Glu
530 535 540

Leu Asp Lys Tyr Thr Met Phe His Tyr Leu Arg Ala Gln Glu Phe Glu
545 550 555 560

His Gly Lys Ser Arg Ile Ala Leu Thr Asn Ser Val Asn Glu Ala Leu
565 570 575

Leu Asn Pro Ser Arg Val Tyr Thr Phe Phe Ser Ser Asp Tyr Val Lys
580 585 590

Lys Val Asn Lys Ala Thr Glu Ala Ala Met Phe Leu Gly Trp Val Glu

595

600

605

Gln Leu Val Tyr Asp Phe Thr Asp Glu Thr Ser Glu Val Ser Thr Thr
610 615 620

Asp Lys Ile Ala Asp Ile Thr Ile Ile Ile Pro Tyr Ile Gly Pro Ala
625 630 635 640

Leu Asn Ile Gly Asn Met Leu Tyr Lys Asp Asp Phe Val Gly Ala Leu
645 650 655

Ile Phe Ser Gly Ala Val Ile Leu Leu Glu Phe Ile Pro Glu Ile Ala
660 665 670

Ile Pro Val Leu Gly Thr Phe Ala Leu Val Ser Tyr Ile Ala Asn Lys
675 680 685

Val Leu Thr Val Gln Thr Ile Asp Asn Ala Leu Ser Lys Arg Asn Glu
690 695 700

Lys Trp Asp Glu Val Tyr Lys Tyr Ile Val Thr Asn Trp Leu Ala Lys
705 710 715 720

Val Asn Thr Gln Ile Asp Leu Ile Arg Lys Lys Met Lys Glu Ala Leu
725 730 735

Glu Asn Gln Ala Glu Ala Thr Lys Ala Ile Ile Asn Tyr Gln Tyr Asn
740 745 750

Gln Tyr Thr Glu Glu Glu Lys Asn Asn Ile Asn Phe Asn Ile Asp Asp
755 760 765

Leu Ser Ser Lys Leu Asn Glu Ser Ile Asn Lys Ala Met Ile Asn Ile
770 775 780

Asn Lys Phe Leu Asn Gln Cys Ser Val Ser Tyr Leu Met Asn Ser Met
785 790 795 800

Ile Pro Tyr Gly Val Lys Arg Leu Glu Asp Phe Asp Ala Ser Leu Lys
805 810 815

Asp Ala Leu Leu Lys Tyr Ile Tyr Asp Asn Arg Gly Thr Leu Ile Gly
820 825 830

Gln Val Asp Arg Leu Lys Asp Lys Val Asn Asn Thr Leu Ser Thr Asp
835 840 845

ALLE0004-100sequencelisting.txt

Ile Pro Phe Gln Leu Ser Lys Tyr Val Asp Asn Gln Arg Leu Leu Ser
850 855 860

Thr Phe Thr Glu Tyr Ile Lys Asn Ile Ile Asn Thr Ser Ile Leu Asn
865 870 875 880

Leu Arg Tyr Glu Ser Asn His Leu Ile Asp Leu Ser Arg Tyr Ala Ser
885 890 895

Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp Pro Ile Asp Lys Asn
900 905 910

Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys Ile Glu Val Ile Leu
915 920 925

Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe Ser Thr Ser
930 935 940

Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser Ile Ser Leu Asn Asn
945 950 955 960

Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn Ser Gly Trp Lys Val
965 970 975

Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu Gln Asp Thr Gln Glu
980 985 990

Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln Met Ile Asn Ile Ser
995 1000 1005

Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile Thr Asn Asn Arg
1010 1015 1020

Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu Ile Asp Gln
1025 1030 1035

Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn Asn Ile
1040 1045 1050

Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile Trp
1055 1060 1065

Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu
1070 1075 1080

Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys
1085 1090 1095

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Asp Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met
1100 1105 1110

Leu Asn Leu Tyr Asp Pro Asn Lys Tyr Val Asp Val Asn Asn Val
1115 1120 1125

Gly Ile Arg Gly Tyr Met Tyr Leu Lys Gly Pro Arg Gly Ser Val
1130 1135 1140

Met Thr Thr Asn Ile Tyr Leu Asn Ser Ser Leu Tyr Arg Gly Thr
1145 1150 1155

Lys Phe Ile Ile Lys Lys Tyr Ala Ser Gly Asn Lys Asp Asn Ile
1160 1165 1170

Val Arg Asn Asn Asp Arg Val Tyr Ile Asn Val Val Val Lys Asn
1175 1180 1185

Lys Glu Tyr Arg Leu Ala Thr Asn Ala Ser Gln Ala Gly Val Glu
1190 1195 1200

Lys Ile Leu Ser Ala Leu Glu Ile Pro Asp Val Gly Asn Leu Ser
1205 1210 1215

Gln Val Val Val Met Lys Ser Lys Asn Asp Gln Gly Ile Thr Asn
1220 1225 1230

Lys Cys Lys Met Asn Leu Gln Asp Asn Asn Gly Asn Asp Ile Gly
1235 1240 1245

Phe Ile Gly Phe His Gln Phe Asn Asn Ile Ala Lys Leu Val Ala
1250 1255 1260

Ser Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser Arg Thr Leu
1265 1270 1275

Gly Cys Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp Gly Glu
1280 1285 1290

Arg Pro Leu
1295

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<223> Peptide fragment (residues 167-177)

<400> 6

Ser Phe Gly His Glu Val Leu Asn Leu Thr Arg
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<210> 7

<211> 12

<212> PRT

<213> Artificial sequence

<220>

<223> Peptide fragment (residues 382-393)

<400> 7

Val Asn Tyr Thr Ile Tyr Asp Gly Phe Asn Leu Arg
1 5 10

<210> 8

<211> 22

<212> PRT

<213> Artificial sequence

<220>

<223> Peptide fragment (residues 394-415)

<400> 8

Asn Thr Asn Leu Ala Ala Asn Phe Asn Gly Gln Asn Thr Glu Ile Asn
1 5 10 15

Asn Met Asn Phe Thr Lys
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<210> 9

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide fragment (residues 418-427)

<400> 9

Asn Phe Thr Gly Leu Phe Glu Phe Tyr Lys
1 5 10

<210> 10

<211> 21

<212> PRT

<213> Artificial sequence

<220>

<223> Peptide fragment (residues 457-477)

<400> 10

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Val Asn Asn Trp Asp Leu Phe Phe Ser Pro Ser Glu Asp Asn Phe Thr
1 5 10 15

Asn Asp Leu Asn Lys
20

<210> 11
<211> 59
<212> PRT
<213> Artificial sequence

<220>
<223> Peptide fragment (residues 478-536)

<400> 11

Gly Glu Glu Ile Thr Ser Asp Thr Asn Ile Glu Ala Ala Glu Glu Asn
1 5 10 15

Ile Ser Leu Asp Leu Ile Gln Gln Tyr Tyr Leu Thr Phe Asn Phe Asp
20 25 30

Asn Glu Pro Glu Asn Ile Ser Ile Glu Asn Leu Ser Ser Asp Ile Ile
35 40 45

Gly Gln Leu Glu Leu Met Pro Asn Ile Glu Arg
50 55

<210> 12
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide fragment (residues 773-779)

<400> 12

Leu Asn Glu Ser Ile Asn Lys
1 5

<210> 13
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide fragment (residues 787-806)

<400> 13

Phe Leu Asn Gln Cys Ser Val Ser Tyr Leu Met Asn Ser Met Ile Pro
1 5 10 15

Tyr Gly Val Lys
20

<210> 14
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide fragment (residues 841-855)

<400> 14

Val Asn Asn Thr Leu Ser Thr Asp Ile Pro Phe Gln Leu Ser Lys
1 5 10 15

<210> 15
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide fragment (residues 872-882)

<400> 15

Asn Ile Ile Asn Thr Ser Ile Leu Asn Leu Arg
1 5 10

<210> 16
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide fragment (residues 930-948)

<400> 16

Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe Ser Thr Ser Phe
1 5 10 15

Trp Ile Arg

<210> 17
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide fragment (residues 952-975)

<400> 17

Tyr Phe Asn Ser Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys
1 5 10 15

Met Glu Asn Asn Ser Gly Trp Lys

20

<210> 18
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Peptide fragment (residues 1001-1013)

<400> 18

Tyr Ser Gln Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg
 1 5 10

<210> 19
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Peptide fragment (residues 1024-1028)

<400> 19

Leu Asn Asn Ser Lys
 1 5

<210> 20
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Peptide fragment (residues 1086-1098)

<400> 20

Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys
 1 5 10

<210> 21
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Peptide fragment (residues 1141-1156)

<400> 21

Gly Ser Val Met Thr Thr Asn Ile Tyr Leu Asn Ser Ser Leu Tyr Arg
 1 5 10 15

<210> 22
 <211> 12
 <212> PRT

<213> Artificial Sequence

<220>

<223> Peptide fragment (residues 1193-1204)

<400> 22

Leu Ala Thr Asn Ala Ser Gln Ala Gly Val Glu Lys
1 5 10

<210> 23

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide fragment (residues 1205-1224)

<400> 23

Ile Leu Ser Ala Leu Glu Ile Pro Asp Val Gly Asn Leu Ser Gln Val
1 5 10 15

Val Val Met Lys
20

<210> 24

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide fragment (residues 1261-1269)

<400> 24

Leu Val Ala Ser Asn Trp Tyr Asn Arg
1 5

<210> 25

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide fragment (residues 20-40)

<400> 25

Val Asn Asn Trp Asp Leu Phe Phe Ser Pro Ser Glu Asp Asn Phe Thr
1 5 10 15

Asn Asp Leu Asn Lys
20

<210> 26

<211> 59

<212> PRT

<213> Artificial Sequence

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<220>

<223> Peptide fragment (residues 41-99)

<400> 26

Gly Glu Glu Ile Thr Ser Asp Thr Asn Ile Glu Ala Ala Glu Glu Asn
 1 5 10 15
 Ile Ser Leu Asp Leu Ile Gln Gln Tyr Tyr Leu Thr Phe Asn Phe Asp
 20 25 30
 Asn Glu Pro Glu Asn Ile Ser Ile Glu Asn Leu Ser Ser Asp Ile Ile
 35 40 45
 Gly Gln Leu Glu Leu Met Pro Asn Ile Glu Arg
 50 55

<210> 27

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide fragment (residues 336-342)

<400> 27

Leu Asn Glu Ser Ile Asn Lys
 1 5

<210> 28

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide fragment (residues 350-369)

<400> 28

Phe Leu Asn Gln Cys Ser Val Ser Tyr Leu Met Asn Ser Met Ile Pro
 1 5 10 15
 Tyr Gly Val Lys
 20

<210> 29

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide fragment (residues 404-418)

<400> 29

Val Asn Asn Thr Leu Ser Thr Asp Ile Pro Phe Gln Leu Ser Lys
 1 5 10 15

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<210> 30
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Peptide fragment (residues 435-445)

<400> 30

Asn Ile Ile Asn Thr Ser Ile Leu Asn Leu Arg
 1 5 10

<210> 31
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Peptide fragment (residues 493-511)

<400> 31

Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe Ser Thr Ser Phe
 1 5 10 15

Trp Ile Arg

<210> 32
 <211> 24
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Peptide fragment (residues 515-538)

<400> 32

Tyr Phe Asn Ser Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys
 1 5 10 15

Met Glu Asn Asn Ser Gly Trp Lys
 20

<210> 33
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Peptide fragment (residues 564-576)

<400> 33

Tyr Ser Gln Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg
 1 5 10

<210> 34
 <211> 5
 <212> PRT
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<220>
 <223> Peptide fragment (residues 587-591)

<400> 34

Leu Asn Asn Ser Lys
 1 5

<210> 35
 <211> 13
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 <213> Artificial Sequence

<220>
 <223> Peptide fragment (residues 649-661)

<400> 35

Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys
 1 5 10

<210> 36
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Peptide fragment (residues 704-719)

<400> 36

Gly Ser Val Met Thr Thr Asn Ile Tyr Leu Asn Ser Ser Leu Tyr Arg
 1 5 10 15

<210> 37
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 <212> PRT
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<220>
 <223> Peptide fragment (residues 756-767)

<400> 37

Leu Ala Thr Asn Ala Ser Gln Ala Gly Val Glu Lys
 1 5 10

<210> 38
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Peptide fragment (residues 768-787)

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<400> 38

Ile Leu Ser Ala Leu Glu Ile Pro Asp Val Gly Asn Leu Ser Gln Val
1 5 10 15
Val Val Met Lys
20

<210> 39

<211> 859

<212> PRT

<213> Clostridium botulinum

<400> 39

Lys Thr Lys Ser Leu Asp Lys Gly Tyr Asn Lys Ala Leu Asn Asp Leu
1 5 10 15

Cys Ile Lys Val Asn Asn Trp Asp Leu Phe Phe Ser Pro Ser Glu Asp
20 25 30

Asn Phe Thr Asn Asp Leu Asn Lys Gly Glu Glu Ile Thr Ser Asp Thr
35 40 45

Asn Ile Glu Ala Ala Glu Glu Asn Ile Ser Leu Asp Leu Ile Gln Gln
50 55 60

Tyr Tyr Leu Thr Phe Asn Phe Asp Asn Glu Pro Glu Asn Ile Ser Ile
65 70 75 80

Glu Asn Leu Ser Ser Asp Ile Ile Gly Gln Leu Glu Leu Met Pro Asn
85 90 95

Ile Glu Arg Phe Pro Asn Gly Lys Lys Tyr Glu Leu Asp Lys Tyr Thr
100 105 110

Met Phe His Tyr Leu Arg Ala Gln Glu Phe Glu His Gly Lys Ser Arg
115 120 125

Ile Ala Leu Thr Asn Ser Val Asn Glu Ala Leu Leu Asn Pro Ser Arg
130 135 140

Val Tyr Thr Phe Phe Ser Ser Asp Tyr Val Lys Lys Val Asn Lys Ala
145 150 155 160

Thr Glu Ala Ala Met Phe Leu Gly Trp Val Glu Gln Leu Val Tyr Asp
165 170 175

Phe Thr Asp Glu Thr Ser Glu Val Ser Thr Thr Asp Lys Ile Ala Asp
180 185 190

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Ile Thr Ile Ile Ile Pro Tyr Ile Gly Pro Ala Leu Asn Ile Gly Asn
195 200 205

Met Leu Tyr Lys Asp Asp Phe Val Gly Ala Leu Ile Phe Ser Gly Ala
210 215 220

Val Ile Leu Leu Glu Phe Ile Pro Glu Ile Ala Ile Pro Val Leu Gly
225 230 235 240

Thr Phe Ala Leu Val Ser Tyr Ile Ala Asn Lys Val Leu Thr Val Gln
245 250 255

Thr Ile Asp Asn Ala Leu Ser Lys Arg Asn Glu Lys Trp Asp Glu Val
260 265 270

Tyr Lys Tyr Ile Val Thr Asn Trp Leu Ala Lys Val Asn Thr Gln Ile
275 280 285

Asp Leu Ile Arg Lys Lys Met Lys Glu Ala Leu Glu Asn Gln Ala Glu
290 295 300

Ala Thr Lys Ala Ile Ile Asn Tyr Gln Tyr Asn Gln Tyr Thr Glu Glu
305 310 315 320

Glu Lys Asn Asn Ile Asn Phe Asn Ile Asp Asp Leu Ser Ser Lys Leu
325 330 335

Asn Glu Ser Ile Asn Lys Ala Met Ile Asn Ile Asn Lys Phe Leu Asn
340 345 350

Gln Cys Ser Val Ser Tyr Leu Met Asn Ser Met Ile Pro Tyr Gly Val
355 360 365

Lys Arg Leu Glu Asp Phe Asp Ala Ser Leu Lys Asp Ala Leu Leu Lys
370 375 380

Tyr Ile Tyr Asp Asn Arg Gly Thr Leu Ile Gly Gln Val Asp Arg Leu
385 390 395 400

Lys Asp Lys Val Asn Asn Thr Leu Ser Thr Asp Ile Pro Phe Gln Leu
405 410 415

Ser Lys Tyr Val Asp Asn Gln Arg Leu Leu Ser Thr Phe Thr Glu Tyr
420 425 430

Ile Lys Asn Ile Ile Asn Thr Ser Ile Leu Asn Leu Arg Tyr Glu Ser

435

440

445

Asn His Leu Ile Asp Leu Ser Arg Tyr Ala Ser Lys Ile Asn Ile Gly
450 455 460

Ser Lys Val Asn Phe Asp Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe
465 470 475 480

Asn Leu Glu Ser Ser Lys Ile Glu Val Ile Leu Lys Asn Ala Ile Val
485 490 495

Tyr Asn Ser Met Tyr Glu Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile
500 505 510

Pro Lys Tyr Phe Asn Ser Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile
515 520 525

Asn Cys Met Glu Asn Asn Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly
530 535 540

Glu Ile Ile Trp Thr Leu Gln Asp Thr Gln Glu Ile Lys Gln Arg Val
545 550 555 560

Val Phe Lys Tyr Ser Gln Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg
565 570 575

Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile
580 585 590

Tyr Ile Asn Gly Arg Leu Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly
595 600 605

Asn Ile His Ala Ser Asn Asn Ile Met Phe Lys Leu Asp Gly Cys Arg
610 615 620

Asp Thr His Arg Tyr Ile Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys
625 630 635 640

Glu Leu Asn Glu Lys Glu Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn
645 650 655

Ser Gly Ile Leu Lys Asp Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys
660 665 670

Pro Tyr Tyr Met Leu Asn Leu Tyr Asp Pro Asn Lys Tyr Val Asp Val
675 680 685

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Asn Asn Val Gly Ile Arg Gly Tyr Met Tyr Leu Lys Gly Pro Arg Gly
690 695 700

Ser Val Met Thr Thr Asn Ile Tyr Leu Asn Ser Ser Leu Tyr Arg Gly
705 710 715 720

Thr Lys Phe Ile Ile Lys Lys Tyr Ala Ser Gly Asn Lys Asp Asn Ile
725 730 735

Val Arg Asn Asn Asp Arg Val Tyr Ile Asn Val Val Val Lys Asn Lys
740 745 750

Glu Tyr Arg Leu Ala Thr Asn Ala Ser Gln Ala Gly Val Glu Lys Ile
755 760 765

Leu Ser Ala Leu Glu Ile Pro Asp Val Gly Asn Leu Ser Gln Val Val
770 775 780

Val Met Lys Ser Lys Asn Asp Gln Gly Ile Thr Asn Lys Cys Lys Met
785 790 795 800

Asn Leu Gln Asp Asn Asn Gly Asn Asp Ile Gly Phe Ile Gly Phe His
805 810 815

Gln Phe Asn Asn Ile Ala Lys Leu Val Ala Ser Asn Trp Tyr Asn Arg
820 825 830

Gln Ile Glu Arg Ser Ser Arg Thr Leu Gly Cys Ser Trp Glu Phe Ile
835 840 845

Pro Val Asp Asp Gly Trp Gly Glu Arg Pro Leu
850 855

<210> 40

<211> 18

<212> PRT

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<220>

<223> Peptide fragment (residues 49-66)

<400> 40

Asp Thr Phe Thr Asn Pro Glu Glu Gly Asp Leu Asn Pro Pro Pro Glu
1 5 10 15

Ala Lys

<210> 41

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<211> 18
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Peptide fragment (residues 67-84)

<400> 41

Gln Val Pro Val Ser Tyr Tyr Asp Ser Thr Tyr Leu Ser Thr Asp Asn
 1 5 10 15

Glu Lys

<210> 42
 <211> 4
 <212> PRT
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<220>
 <223> Peptide fragment (residues 90-93)

<400> 42

Gly Val Thr Lys
 1

<210> 43
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Peptide fragment (residues 98-105)

<400> 43

Ile Tyr Ser Thr Asp Leu Gly Arg
 1 5

<210> 44
 <211> 8
 <212> PRT
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<220>
 <223> Peptide fragment (residues 106-113)

<400> 44

Met Leu Leu Thr Ser Ile Val Arg
 1 5

<210> 45
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Peptide fragment (residues 114-128)

<400> 45

Gly Ile Pro Phe Trp Gly Gly Ser Thr Ile Asp Thr Glu Leu Lys
1 5 10 15

<210> 46

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide fragment (residues 129-145)

<400> 46

Val Ile Asp Thr Asn Cys Ile Asn Val Ile Gln Pro Asp Gly Ser Tyr
1 5 10 15

Arg

<210> 47

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide fragment (residues 146-166)

<400> 47

Ser Glu Glu Leu Asn Leu Val Ile Ile Gly Pro Ser Ala Asp Ile Ile
1 5 10 15

Gln Phe Glu Cys Lys
20

<210> 48

<211> 11

<212> PRT

<213> Artificial sequence

<220>

<223> Peptide fragment (residues 167-177)

<400> 48

Ser Phe Gly His Glu Val Leu Asn Leu Thr Arg
1 5 10

<210> 49

<211> 10

<212> PRT

<213> Artificial sequence

<220>

<223> Peptide fragment (residues 178-187)

<400> 49

Asn Gly Tyr Gly Ser Thr Gln Tyr Ile Arg
1 5 10

<210> 50

<211> 25

<212> PRT

<213> Artificial sequence

<220>

<223> Peptide fragment (residues 188-212)

<400> 50

Phe Ser Pro Asp Phe Thr Phe Gly Phe Glu Glu Ser Glu Leu Val Asp
1 5 10 15

Thr Asn Pro Leu Leu Gly Ala Gly Lys
20 25

<210> 51

<211> 19

<212> PRT

<213> Artificial sequence

<220>

<223> Peptide fragment (residues 213-231)

<400> 51

Phe Ala Thr Asp Pro Ala Val Thr Leu Ala His Glu Leu Ile His Ala
1 5 10 15

Gly His Arg

<210> 52

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide fragment (residues 245-264)

<400> 52

Val Asn Thr Asn Ala Tyr Tyr Glu Met Ser Gly Leu Glu Val Ser Phe
1 5 10 15

Glu Glu Leu Arg
20

<210> 53

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide fragment (residues 265-272)

<400> 53

Thr Phe Gly Gly His Asp Ala Lys
1 5

<210> 54

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide fragment (residues 273-283)

<400> 54

Phe Ile Asp Ser Leu Gln Glu Asn Glu Phe Arg
1 5 10

<210> 55

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide fragment (residues 292-299)

<400> 55

Asp Ile Ala Ser Thr Leu Asn Lys
1 5

<210> 56

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide fragment (residues 302-314)

<400> 56

Ser Ile Val Gly Thr Thr Ala Ser Leu Gln Tyr Met Lys
1 5 10

<210> 57

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide fragment (residues 321-330)

<400> 57

Tyr Leu Ser Ser Glu Asp Thr Ser Gly Lys
1 5 10

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<210> 58
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Peptide fragment (residues 331-335)

<400> 58

Phe Ser Val Asp Lys
 1 5

<210> 59
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Peptide fragment (residues 344-356)

<400> 59

Met Leu Thr Glu Ile Tyr Thr Glu Asp Asn Phe Val Lys
 1 5 10

<210> 60
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Peptide fragment (residues 365-371)

<400> 60

Thr Tyr Leu Asn Phe Asp Lys
 1 5

<210> 61
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Peptide fragment (residues 382-393)

<400> 61

Val Asn Tyr Thr Ile Tyr Asp Gly Phe Asn Leu Arg
 1 5 10

<210> 62
 <211> 22
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Peptide fragment (residues 394-415)

<400> 62

Asn Thr Asn Leu Ala Ala Asn Phe Asn Gly Gln Asn Thr Glu Ile Asn
1 5 10 15

Asn Met Asn Phe Thr Lys
20

<210> 63

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide fragment (residues 418-427)

<400> 63

Asn Phe Thr Gly Leu Phe Glu Phe Tyr Lys
1 5 10

<210> 64

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide fragment (residues 433-438)

<400> 64

Gly Ile Ile Thr Ser Lys
1 5

<210> 65

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide fragment (residues 1227-1234)

<400> 65

Asn Asp Gln Gly Ile Thr Asn Lys
1 5

<210> 66

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide fragment (residues 441-444)

<400> 66

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Ser Leu Asp Lys
1

<210> 67
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide fragment (residues 457-477)

<400> 67

Val Asn Asn Trp Asp Leu Phe Phe Ser Pro Ser Glu Asp Asn Phe Thr
1 5 10 15
Asn Asp Leu Asn Lys
20

<210> 68
<211> 59
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide fragment (residues 478-536)

<400> 68

Gly Glu Glu Ile Thr Ser Asp Thr Asn Ile Glu Ala Ala Glu Glu Asn
1 5 10 15
Ile Ser Leu Asp Leu Ile Gln Gln Tyr Tyr Leu Thr Phe Asn Phe Asp
20 25 30
Asn Glu Pro Glu Asn Ile Ser Ile Glu Asn Leu Ser Ser Asp Ile Ile
35 40 45
Gly Gln Leu Glu Leu Met Pro Asn Ile Glu Arg
50 55

<210> 69
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide fragment (residues 548-555)

<400> 69

Tyr Thr Met Phe His Tyr Leu Arg
1 5

<210> 70
<211> 20
<212> PRT
<213> Artificial Sequence

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<220>

<223> Peptide fragment (residues 1205-1224)

<400> 70

Ile Leu Ser Ala Leu Glu Ile Pro Asp Val Gly Asn Leu Ser Gln Val
 1 5 10 15
 Val Val Met Lys
 20

<210> 71

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide fragment (residues 566-581)

<400> 71

Ile Ala Leu Thr Asn Ser Val Asn Glu Ala Leu Leu Asn Pro Ser Arg
 1 5 10 15

<210> 72

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide fragment (residues 582-592)

<400> 72

Val Tyr Thr Phe Phe Ser Ser Asp Tyr Val Lys
 1 5 10

<210> 73

<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide fragment (residues 597-626)

<400> 73

Ala Thr Glu Ala Ala Met Phe Leu Gly Trp Val Glu Gln Leu Val Tyr
 1 5 10 15

Asp Phe Thr Asp Glu Thr Ser Glu Val Ser Thr Thr Asp Lys
 20 25 30

<210> 74

<211> 23

<212> PRT

<213> Artificial Sequence

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<220>

<223> Peptide fragment (residues 627-649)

<400> 74

Ile Ala Asp Ile Thr Ile Ile Ile Pro Tyr Ile Gly Pro Ala Leu Asn
1 5 10 15

Ile Gly Asn Met Leu Tyr Lys
20

<210> 75

<211> 39

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide fragment (residues 650-688)

<400> 75

Asp Asp Phe Val Gly Ala Leu Ile Phe Ser Gly Ala Val Ile Leu Leu
1 5 10 15

Glu Phe Ile Pro Glu Ile Ala Ile Pro Val Leu Gly Thr Phe Ala Leu
20 25 30

Val Ser Tyr Ile Ala Asn Lys
35

<210> 76

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide fragment (residues 689-701)

<400> 76

Val Leu Thr Val Gln Thr Ile Asp Asn Ala Leu Ser Lys
1 5 10

<210> 77

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide fragment (residues 712-720)

<400> 77

Tyr Ile Val Thr Asn Trp Leu Ala Lys
1 5

<210> 78

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide fragment (residues 721-729)

<400> 78

Val Asn Thr Gln Ile Asp Leu Ile Arg
1 5

<210> 79

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide fragment (residues 734-744)

<400> 79

Glu Ala Leu Glu Asn Gln Ala Glu Ala Thr Lys
1 5 10

<210> 80

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide fragment (residues 745-759)

<400> 80

Ala Ile Ile Asn Tyr Gln Tyr Asn Gln Tyr Thr Glu Glu Glu Lys
1 5 10 15

<210> 81

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide fragment (residues 760-772)

<400> 81

Asn Asn Ile Asn Phe Asn Ile Asp Asp Leu Ser Ser Lys
1 5 10

<210> 82

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide fragment (residues 773-779)

<400> 82

Leu Asn Glu Ser Ile Asn Lys
1 5

<210> 83
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide fragment (residues 787-806)

<400> 83

Phe Leu Asn Gln Cys Ser Val Ser Tyr Leu Met Asn Ser Met Ile Pro
1 5 10 15

Tyr Gly Val Lys

<210> 84
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide fragment (residues 808-816)

<400> 84

Leu Glu Asp Phe Asp Ala Ser Leu Lys
1 5

<210> 85
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide fragment (residues 828-836)

<400> 85

Gly Thr Leu Ile Gly Gln Val Asp Arg
1 5

<210> 86
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide fragment (residues 841-855)

<400> 86

Val Asn Asn Thr Leu Ser Thr Asp Ile Pro Phe Gln Leu Ser Lys
1 5 10 15

<210> 87

<211> 10
 <212> PRT
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<220>
 <223> Peptide fragment (residues 862-871)

<400> 87

Leu Leu Ser Thr Phe Thr Glu Tyr Ile Lys
 1 5 10

<210> 88
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Peptide fragment (residues 872-882)

<400> 88

Asn Ile Ile Asn Thr Ser Ile Leu Asn Leu Arg
 1 5 10

<210> 89
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Peptide fragment (residues 883-893)

<400> 89

Tyr Glu Ser Asn His Leu Ile Asp Leu Ser Arg
 1 5 10

<210> 90
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 <212> PRT
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<220>
 <223> Peptide fragment (residues 894-897)

<400> 90

Tyr Ala Ser Lys
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<210> 91
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Peptide fragment (residues 898-903)

<400> 91

Ile Asn Ile Gly Ser Lys
1 5

<210> 92

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide fragment (residues 912-923)

<400> 92

Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys
1 5 10

<210> 93

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide fragment (residues 930-948)

<400> 93

Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe Ser Thr Ser Phe
1 5 10 15

Trp Ile Arg

<210> 94

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide fragment (residues 952-975)

<400> 94

Tyr Phe Asn Ser Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys
1 5 10 15

Met Glu Asn Asn Ser Gly Trp Lys
20

<210> 95

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide fragment (residues 976-994)

<400> 95

Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu Gln Asp Thr Gln
1 5 10 15

Glu Ile Lys

<210> 96
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide fragment (residues 1001-1013)

<400> 96

Tyr Ser Gln Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg
1 5 10

<210> 97
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide fragment (residues 1014-1023)

<400> 97

Trp Ile Phe Val Thr Ile Thr Asn Asn Arg
1 5 10

<210> 98
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide fragment (residues 1024-1028)

<400> 98

Leu Asn Asn Ser Lys
1 5

<210> 99
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide fragment (residues 1035-1056)

<400> 99

Leu Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser
1 5 10 15

Asn Asn Ile Met Phe Lys
20

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<210> 100
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 <212> PRT
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<220>
 <223> Peptide fragment (residues 1062-1065)

<400> 100

Asp Thr His Arg
 1

<210> 101
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Peptide fragment (residues 1086-1098)

<400> 101

Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys
 1 5 10

<210> 102
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Peptide fragment (residues 1141-1156)

<400> 102

Gly Ser Val Met Thr Thr Asn Ile Tyr Leu Asn Ser Ser Leu Tyr Arg
 1 5 10 15

<210> 103
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Peptide fragment (residues 1193-1204)

<400> 103

Leu Ala Thr Asn Ala Ser Gln Ala Gly Val Glu Lys
 1 5 10

<210> 104
 <211> 6
 <212> PRT
 <213> Artificial Sequence

ALLE0004-100sequencelisting.txt

<220>

<223> Peptide fragment (residues 1165-1170)

<400> 104

Tyr Ala Ser Gly Asn Lys
1 5

<210> 105

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide fragment (residues 1277-1296)

<400> 105

Thr Leu Gly Cys Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp Gly
1 5 10 15

Glu Arg Pro Leu
20

<210> 106

<211> 4

<212> PRT

<213> BOTULINUM TOXIN

<400> 106

Asn Leu Thr Arg
1

<210> 107

<211> 4

<212> PRT

<213> BOTULINUM TOXIN

<400> 107

Asn Tyr Thr Ile
1

<210> 108

<211> 4

<212> PRT

<213> BOTULINUM TOXIN

<400> 108

Asn Phe Thr Lys
1

<210> 109

<211> 4

<212> PRT

<213> BOTULINUM TOXIN

<400> 109

Asn Phe Thr Gly
1

<210> 110
<211> 4
<212> PRT
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<400> 110

Asn Asn Ser Gly
1

<210> 111
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<400> 111

Asn Ile Ser Asp
1

<210> 112
<211> 4
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<400> 112

Asn Ala Ser Gln
1

<210> 113
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<400> 113

Asn Leu Ser Gln
1

<210> 114
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<400> 114

Asn Leu Ser Gly
1

<210> 115

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<400> 115

Asn Gly Ser Gly
 1

<210> 116
 <211> 4
 <212> PRT
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<400> 116

Asn Ser Ser Asn
 1

<210> 117
 <211> 4
 <212> PRT
 <213> BOTULINUM TOXIN

<400> 117

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